

The human haplotype map and its application to Genetics of Disease.

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A new map of common individual gene variations, the human haplotype map (www.hapmap.org), has been added to the map of the human genome to provide a critical tool for identifying the vulnerability genes involved in genetically complex diseases such as hypertension, diabetes, cancer and neuropsychiatric disorders. Most individual variations are present as common single nucleotide polymorphisms (SNPs), which have been estimated in a number of 10 million in the normal population, and recently identified entirely by the Hapmap project. A haplotype is known as a set of SNP alleles along a region of a chromosome. In theory, a lot of haplotypes could exist in a given chromosome region, although studies have only found few common haplotypes. According to Dr. Gabriel, if limiting the genetic scan to just 10 million SNPs, instead of the whole human genome, represents a gain in efficiency, more can be achieved if associations between SNP alleles are explored. The principal aim of the Hapmap project is to build a public database of common patterns of genetic variants in the human genome using populations of reference. Currently, is it possible to find patterns of sequence variations across genes and identify which SNPs are the best to genotype. If, lets say, 300,000 SNPs are appropriately selected, it would be possible to identify 90% of the common variations, alleviating the necessity of sequencing the entire genome or genotype 10 million SNPs. The Hapmap project was designed to produce data with enough quality and cost-efficiency to perform large scale association studies. Standard SNP panels are commercially available today, allowing the performance of hundreds of thousands essays in parallel, at a rate of ~ \$1,000 per sample, making whole genome association scans more feasible than ever. Association studies in the past were generally based on one or several candidate genes, an approach that undeniably generate scientific bias, not to mention the waist of resources, but whole genome scans for association studies are now practical thanks to the availability of public databases of common variations such as Hapmap. Identifying genetic variations associated with disease may provide new clues in pathophysiology, and reveal potential therapeutic targets. The complete human genome, the Hapmap project and technological advances combined together yield a novel approach to understand the risk generated by common variations in the genome, and ultimately to design possible strategies for preventive interventions.